

1642

RAW SEQUENCE LISTING

DATE: 10/15/2001

PATENT APPLICATION: US/09/559,013B

TIME: 13:41:18

Input Set : A:\561389_1.txt

Output Set: N:\CRF3\10152001\I559013B.raw

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3 <110> APPLICANT: Ono, Toshiro
4   Nakayama, Eiichi
6 <120> TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
7   THEREFOR
9 <130> FILE REFERENCE: L0461/7086
11 <140> CURRENT APPLICATION NUMBER: US 09/559,013B
12 <141> CURRENT FILING DATE: 2000-04-26
14 <150> PRIOR APPLICATION NUMBER: US 60/168,353
15 <151> PRIOR FILING DATE: 1999-12-01
17 <160> NUMBER OF SEQ ID NOS: 32
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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22 <211> LENGTH: 538
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus musculus
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28   tatctgcgtc ggggagagcg gagacagact gacccgggca gccaaaggtgt tggagcagct      120
29   cacaggccag accccggtgt tctccaaagc tagatacact gtcaggctct ttggcatccg      180
30   gagaaaatgag aagattgctg ttcactgcac agtccgcgga gccaaaggcag aggaaattct      240
31   ggagaaaaggc ctgaaggtgc gggagtatga gttgcggaaa aataacttct cggatactgg      300
32   aaactttggt tttggaattc aagaacacat tgacctgggc atcaaatacg acccaagcat      360
33   tgggatctac ggcctggact tctatgtggt gctgggtagg ccagggttca gcatcgcaga      420
34   caagaagcgc agaacaggct gcattggggc caaacacaga atcagcaagg aggaggccat      480
35   gcgctgggtc cagcagaagt acgatggaat catccttcct ggaaaaataaa cttgatcc      538
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 175
39 <212> TYPE: PRT
40 <213> ORGANISM: Mus musculus
42 <400> SEQUENCE: 2
43   Asp Gln Gly Glu Lys Glu Asn Pro Met Arg Glu Leu Arg Ile Arg Lys
44   1           5           10           15
45   Leu Cys Leu Asn Ile Cys Val Gly Glu Ser Gly Asp Arg Leu Thr Arg
46           20           25           30
47   Ala Ala Lys Val Leu Glu Gln Leu Thr Gly Gln Thr Pro Val Phe Ser
48           35           40           45
49   Lys Ala Arg Tyr Thr Val Arg Ser Phe Gly Ile Arg Arg Asn Glu Lys
50           50           55           60
51   Ile Ala Val His Cys Thr Val Arg Gly Ala Lys Ala Glu Glu Ile Leu
52           65           70           75           80
53   Glu Lys Gly Leu Lys Val Arg Glu Tyr Glu Leu Arg Lys Asn Asn Phe
54           85           90           95
55   Ser Asp Thr Gly Asn Phe Gly Phe Gly Ile Gln Glu His Ile Asp Leu
56           100          105          110
57   Gly Ile Lys Tyr Asp Pro Ser Ile Gly Ile Tyr Gly Leu Asp Phe Tyr
58           115          120          125
59   Val Val Leu Gly Arg Pro Gly Phe Ser Ile Ala Asp Lys Lys Arg Arg

```

Edit and process

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60      130      135      140
61 Thr Gly Cys Ile Gly Ala Lys His Arg Ile Ser Lys Glu Glu Ala Met
62 145      150      155      160
63 Arg Trp Phe Gln Gln Lys Tyr Asp Gly Ile Ile Leu Pro Gly Lys
64      165      170      175
66 <210> SEQ ID NO: 3
67 <211> LENGTH: 1228
68 <212> TYPE: DNA
69 <213> ORGANISM: Mus musculus
71 <400> SEQUENCE: 3
72 acagccgcat cttcttgtgc agtgccagcc tcgtcccgtg gacaaaatgg tgaaggctcg 60
73 tgtgaacgga tttggccgta ttgggcgcct ggtcaccagg gctgccattt gcagtggcaa 120
74 agtggagatt gttgccatca acgacccctt cattgacctc aactacatgg tctacatgtt 180
75 ccagtatgac tccactcacg gcaaattcaa cggcacagtc aaggccgaga atgggaagct 240
76 tgtcatcaac gggaagccca tcaccatctt ccaggagcga gaccccaacta acatcaaattg 300
77 ggggtgaggcc ggtgctgagt atgtcgtgga gtctactggt gtcttcacca ccatggagaa 360
78 ggccggggcc cacttgaagg gtggagccaa acgggtcatc atctccgccc cttctgccga 420
79 tgcccccattg tttgtgatgg gtgtgaacca cgagaaatat gacaactcac tcaagattgt 480
80 cagcaatgca tcctgcacca ccaactgctt agcccccttg gccaaaggtca tccatgacaa 540
81 ctttggcatt gtggaagggc tcatgaccac agtccatgcc atcactgcca cccagaagac 600
82 tgtggatggc ccctctggaa agctgtggcg tgatggccgt ggggctgccc agaacatcat 660
83 ccctgcatcc actggtgctg ccaaggctgt gggcaaggtc atcccagagc tgaacgggaa 720
84 gctcactggc atggccttcc gtgttcttac cccaatgtg tccgtcgttg atctgacgtg 780
85 ccgcttgag aaacctgcca agtatgatga catcaagaag gtggtgaagc aggcatttga 840
86 gggcccactg aagggcatct tgggctacac tgaggaccag gttgtctct gcgacttcaa 900
87 cagcaactcc cactcttcca ccttcgatgc cggggctggc attgctctca atgacaactt 960
88 tgtcaagctc atttctctgt atgacaatga atacggctac agcaacaggg tgggtggacct 1020
89 catggcctac atggcctcca aggagtaaga aacctggac caccaccccc agcaaggaca 1080
90 ctgagcaaga gaggccctat cccaactcgg cccccaacac tgagcatctc cctcacaatt 1140
91 tccatcccag acccccataa taacaggagg ggcctaggga gccctcccta ctctcttgaa 1200
92 taccatcaat aaagtctcgt gcacccac
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95 <211> LENGTH: 333
96 <212> TYPE: PRT
97 <213> ORGANISM: Mus musculus
99 <400> SEQUENCE: 4
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101 1      5      10      15
102 Thr Arg Ala Ala Ile Cys Ser Gly Lys Val Glu Ile Val Ala Ile Asn
103      20      25      30
104 Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp
105      35      40      45
106 Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu Asn Gly Lys
107      50      55      60
108 Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro
109      65      70      75      80
110 Thr Asn Ile Lys Trp Gly Glu Ala Gly Ala Glu Tyr Val Val Glu Ser
111      85      90      95
112 Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Lys Gly

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113          100          105          110
114 Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met
115          115          120          125
116 Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile
117          130          135          140
118 Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys
119          145          150          155          160
120 Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val
121          165          170          175
122 His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys
123          180          185          190
124 Leu Trp Arg Asp Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser
125          195          200          205
126 Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly
127          210          215          220
128 Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val
129          225          230          235          240
130 Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile
131          245          250          255
132 Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu
133          260          265          270
134 Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser Asn Ser
135          275          280          285
136 His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp Asn
137          290          295          300
138 Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser Asn
139          305          310          315          320
140 Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser Lys Glu
141          325          330

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143 <210> SEQ ID NO: 5

144 <211> LENGTH: 1705

145 <212> TYPE: DNA

146 <213> ORGANISM: Mus musculus

Edit and process

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W--> 148 <220> FEATURE: <221> Unsure <222> (730)..(730) <223> n = a, c, g, or t
W--> 148 <220> FEATURE: <221> Unsure <222> (730)..(730) <223> n = a, c, g, or t
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W--> 149 <220> FEATURE: <221> Unsure <222> (746)..(746) <223> n = a, c, g, or t
W--> 151 <220> FEATURE: <221> Unsure <222> (755)..(755) <223> n = a, c, g, or t
W--> 152 <220> FEATURE: <221> Unsure <222> (1288)..(1288) <223> n = a, c, g, or t
W--> 152 <220> FEATURE: <221> Unsure <222> (1288)..(1288) <223> n = a, c, g, or t
W--> 153 <220> FEATURE: <221> Unsure <222> (1318)..(1318) <223> n = a, c, g, or t
W--> 153 <220> FEATURE: <221> Unsure <222> (1318)..(1318) <223> n = a, c, g, or t
W--> 154 <220> FEATURE: <221> Unsure <222> (1360)..(1360) <223> n = a, c, g, or t
W--> 154 <220> FEATURE: <221> Unsure <222> (1360)..(1360) <223> n = a, c, g, or t
156 <400> SEQUENCE: 5
157 gccgcgggtga gggaagtga cgcgatggcc gggtcgcgct ggggtgtccaa ggtctctcgg 60
158 ctgctgggtg cattccacaa cacaaaacag gtgacaagag gttttgctgg tgggtgttcag 120

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159 acagtaactt taattcctgg agatggaatt ggcccagaaa tttcagcctc agtcatgaag 180
160 atttttgatg ctgccaaagc acctattcag tgggaggagc gcaatgtcac agcaattcaa 240
161 ggaccaggag gaaagtggat gatccctcca gaagccaagg agtccatgga taagaacaag 300
162 atgggcttga aaggccact aaagacccca atagccgctg gccatccatc tatgaatctg 360
163 ttgcttcgta agacatttga cttttatgcc aatgtccggc catgtgtctc aattgaaggt 420
164 tataaaaccc cttacacgga tgtaaataatc gtcaccatcc gagagaacac ggaaggagaa 480
165 tacagtggaa ttgagcatgt gatcgttgat ggggttggtc agagcatcaa gctcatcacc 540
166 gaagaagcaa gcaagcgcat tgcagagttt gcttcgagta cgctcggaac aaccaccgga 600
W--> 167 accacgtcac ngctgtgcac aaaagctaac atcatgagga tgtcagatgg gctctttctg 660
168 caaaaatgca gggaaatttg cggaagaact gtaaagactt aaatttaacg agatgtactt 720
W--> 169 ggatactgtn gtttaaataat gggtaanaag acccntccaa tttgatgttc ttgtcatgcc 780
170 aaattttatac ggagacatcc ttagtgatct gtgtgcagga ctgattggag gtcttgggggt 840
171 gactccaagt ggcaatattg gagccaacgg tgttgccatc tttgaatcgg ttcattggaac 900
172 agccccggac attgcaggca aggacatggc caaccccacg gccctcctgc ttagtgctgt 960
173 gatgatgctt cgccacatgg gactttttga ccatgcagca aaaatcgagg ctgcatgttt 1020
174 tgctacaatt aaggatggaa agagcttaac aaaagatctg ggaggcaacg cgaagtgtc 1080
175 tgacttcaca gaagaaatct gtcgtagagt caaagactta gattagcact cctgctggtg 1140
176 gatttgctgc agtcagtcaa tcaactccaa aggataccct gtaatcctcc ttgagggcgc 1200
177 ccaccattgg tttgcttgggt tcttgacaga gtacgttttt tgaatctggc cttttcttaa 1260
W--> 178 caaaaccctt tgcaatggat gcacatgntg gccccaggcc tttcattcaa aaggtttncc 1320
W--> 179 ccaagtgtcg gtgggtattta ttgtcccgtc tgggtaaaacn ttattttgtta aactgtaagt 1380
180 gaactgtatc atttatcatt gttaccccat ttacacttc aggcaaaatc attttcctca 1440
181 actgtaaata ttctgataca gaattaataa gagaagatat ttaacttttt aacaaaagcc 1500
182 ctggattttt ggtttatgaa aaacaaactg ggaataaaac aggggtttta caatcgaca 1560
183 agataacatt attctaatac taatgggtac aaaagaaatt tactgggaaa gttcacagca 1620
184 aaaaaatggg atatttctta aaaatatgga aataaagtat ttgtcctata catgaattac 1680
185 tattaataaaa aatgtaagct ccaag 1705
187 <210> SEQ ID NO: 6
188 <211> LENGTH: 233
189 <212> TYPE: PRT
190 <213> ORGANISM: Mus musculus
192 <220> FEATURE:
193 <221> NAME/KEY: UNSURE
194 <222> LOCATION: (204)..(204)
195 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 196 <400> SEQUENCE: 6
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198 1 5 10 15
199 Lys Val Ser Arg Leu Leu Gly Ala Phe His Asn Thr Lys Gln Val Thr
200 20 25 30
201 Arg Gly Phe Ala Gly Gly Val Gln Thr Val Thr Leu Ile Pro Gly Asp
202 35 40 45
203 Gly Ile Gly Pro Glu Ile Ser Ala Ser Val Met Lys Ile Phe Asp Ala
204 50 55 60
205 Ala Lys Ala Pro Ile Gln Trp Glu Glu Arg Asn Val Thr Ala Ile Gln
206 65 70 75 80
207 Gly Pro Gly Gly Lys Trp Met Ile Pro Pro Glu Ala Lys Glu Ser Met
208 85 90 95
209 Asp Lys Asn Lys Met Gly Leu Lys Gly Pro Leu Lys Thr Pro Ile Ala

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```

210          100          105          110
211 Ala Gly His Pro Ser Met Asn Leu Leu Leu Arg Lys Thr Phe Asp Leu
212          115          120          125
213 Tyr Ala Asn Val Arg Pro Cys Val Ser Ile Glu Gly Tyr Lys Thr Pro
214          130          135          140
215 Tyr Thr Asp Val Asn Ile Val Thr Ile Arg Glu Asn Thr Glu Gly Glu
216          145          150          155          160
217 Tyr Ser Gly Ile Glu His Val Ile Val Asp Gly Val Val Gln Ser Ile
218          165          170          175
219 Lys Leu Ile Thr Glu Glu Ala Ser Lys Arg Ile Ala Glu Phe Ala Ser
220          180          185          190
W--> 221 Ser Thr Leu Gly Thr Thr Thr Gly Thr Thr Ser Xaa Leu Cys Thr Lys
222          195          200          205
223 Ala Asn Ile Met Arg Met Ser Asp Gly Leu Phe Leu Gln Lys Cys Arg
224          210          215          220
225 Glu Ile Cys Gly Arg Thr Val Lys Thr
226 225          230
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229 <211> LENGTH: 853
230 <212> TYPE: DNA
231 <213> ORGANISM: Mus musculus
233 <400> SEQUENCE: 7
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236 ttccagccgc aaggtcacca ggctactccg cctgggagtc aaggaagact cggaagaaca      180
237 gcatgatgtg aaagcagagg ctttcttcca ggctggagag gggagagatg agcaagggtg      240
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244 gatcaggagg gctgcggcaa gaagaaccag gaggagggca acaccagtcc ctgaacattt      660
245 tagaggaaca ttgagtgtc ctgcttgctg tggagtgaga tggggagaaa gatgcccttt      720
246 tgcgacaccg agattttgat ttgatcacat atgccggcta tgacagccct tacttttcaa      780
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248 aaaatattga tac      853
250 <210> SEQ ID NO: 8
251 <211> LENGTH: 210
252 <212> TYPE: PRT
253 <213> ORGANISM: Mus musculus
255 <400> SEQUENCE: 8
256 Met Glu Ala Glu Gly Ser Ser Arg Lys Val Thr Arg Leu Leu Arg Leu
257 1          5          10          15
258 Gly Val Lys Glu Asp Ser Glu Glu Gln His Asp Val Lys Ala Glu Ala
259          20          25          30
260 Phe Phe Gln Ala Gly Glu Gly Arg Asp Glu Gln Gly Ala Gln Gly Gln
261          35          40          45
262 Pro Gly Val Gly Ala Val Gly Thr Glu Gly Glu Gly Glu Glu Leu Asn

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VERIFICATION SUMMARY

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Input Set : A:\561389_1.txt

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L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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Input Set : A:\561389_1.txt

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L:326 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:327 M:283 W: Missing Blank Line separator, <220> field identifier
L:327 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:339 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:339 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:339 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9

VERIFICATION SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/559,013B

TIME: 13:41:19

Input Set : A:\561389_1.txt

Output Set: N:\CRF3\10152001\I559013B.raw

L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:340 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:341 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:341 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:342 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:342 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:342 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:343 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:344 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:344 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:344 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:535 M:283 W: Missing Blank Line separator, <220> field identifier
L:535 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:536 M:283 W: Missing Blank Line separator, <400> field identifier
L:538 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:538 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:538 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:538 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15

STATISTICS SUMMARY

DATE: 10/15/2001

PATENT APPLICATION: US/09/559,013B

TIME: 13:41:19

Input Set : A:\561389_1.txt

Output Set: N:\CRF3\10152001\I559013B.raw

Application Serial Number: US/09/559,013B

Alpha or Numeric: Numeric

Application Class:

Application File Date: 04-26-2000

Art Unit: 1642

Software Application: FastSeq

Total Number of Sequences: 32

Total Nucleotides: 11930

Total Amino Acids: 2684

Number of Errors: 0

Number of Warnings: 125

Number of Corrections: 0

MESSAGE SUMMARY

256 W: 42 (Invalid Numeric Header Field)

258 W: 33 (Mandatory Feature missing)

283 W: 38 (Missing Blank Line separator)

341 W: 12 ((46) "n" or "Xaa" used)